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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/538,036DATE: 04/18/2000
TIME: 17:29:35

Input Set: I538036.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

ENTERED

1 <110> APPLICANT: Gerald, Christophe P.G.
2 Jones, Kenneth A.
3 Bonini, James A.
4 Borowsky, Beth E.
5 Craig, Douglas A.
6 <120> TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors
7 And Uses Thereof
8 <130> FILE REFERENCE: 57155-D/JPW
9 <140> CURRENT APPLICATION NUMBER: US/09/538,036
10 <141> CURRENT FILING DATE: 2000-03-29
11 <150> EARLIER APPLICATION NUMBER: 09/405,558
12 <151> EARLIER FILING DATE: 1999-09-24
13 <150> EARLIER APPLICATION NUMBER: 09/255,368
14 <151> EARLIER FILING DATE: 1999-02-22
15 <150> EARLIER APPLICATION NUMBER: 09/161,113
16 <151> EARLIER FILING DATE: 1998-09-25
17 <160> NUMBER OF SEQ ID NOS: 71
18 <170> SOFTWARE: PatentIn Ver. 2.1
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20 <211> LENGTH: 1410
21 <212> TYPE: DNA
22 <213> ORGANISM: Rattus norvegicus
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26 cagaacggga gtgatgtgga gaccagcatg gcaaccagcc tcaccttctc ctctactac 180
27 caaactcct ctccggtggc agcatgttc atcgcgccct acgtgctcat ctctctctc 240
28 tgcattggtg gcaacaccct ggtctgcttc attgtgtca agaaccggca catgcgcact 300
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33 aaggcgctgt tcaccatcgc ggtgatctg gctctggcgc tgctcatcat gtgtccctcg 600
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37 gtgcgcatcg cgcgcaagct atgccaggcc cccggtcctg cgcgcgacac ggaggaggcg 840
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44 gacgtgcaac ccagcgactc cggcctgcca tcagagtctg gccccagcag cgggggtccca 1260

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51 <213> ORGANISM: Rattus norvegicus

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57 Ser Ser Tyr Tyr Gln His Ser Ser Pro Val Ala Ala Met Phe Ile Ala
58 35 40 45
59 Ala Tyr Val Leu Ile Phe Leu Leu Cys Met Val Gly Asn Thr Leu Val
60 50 55 60
61 Cys Phe Ile Val Leu Lys Asn Arg His Met Arg Thr Val Thr Asn Met
62 65 70 75 80
63 Phe Ile Leu Asn Leu Ala Val Ser Asp Leu Leu Val Gly Ile Phe Cys
64 85 90 95
65 Met Pro Thr Thr Leu Val Asp Asn Leu Ile Thr Gly Trp Pro Phe Asp
66 100 105 110
67 Asn Ala Thr Cys Lys Met Ser Gly Leu Val Gln Gly Met Ser Val Ser
68 115 120 125
69 Ala Ser Val Phe Thr Leu Val Ala Ile Ala Val Glu Arg Phe Arg Cys
70 130 135 140
71 Ile Val His Pro Phe Arg Glu Lys Leu Thr Leu Arg Lys Ala Leu Phe
72 145 150 155 160
73 Thr Ile Ala Val Ile Trp Ala Leu Ala Leu Ile Met Cys Pro Ser
74 165 170 175
75 Ala Val Thr Leu Thr Val Thr Arg Glu Glu His His Phe Met Leu Asp
76 180 185 190
77 Ala Arg Asn Arg Ser Tyr Pro Leu Tyr Ser Cys Trp Glu Ala Trp Pro
78 195 200 205
79 Glu Lys Gly Met Arg Lys Val Tyr Thr Ala Val Leu Phe Ala His Ile
80 210 215 220
81 Tyr Leu Val Pro Leu Ala Leu Ile Val Val Met Tyr Val Arg Ile Ala
82 225 230 235 240
83 Arg Lys Leu Cys Gln Ala Pro Gly Pro Ala Arg Asp Thr Glu Glu Ala
84 245 250 255
85 Val Ala Glu Gly Gly Arg Thr Ser Arg Arg Arg Ala Arg Val Val His
86 260 265 270
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88 275 280 285
89 Trp Val Leu Leu Leu Leu Ile Asp Tyr Gly Glu Leu Ser Glu Leu Gln
90 290 295 300
91 Leu His Leu Leu Ser Val Tyr Ala Phe Pro Leu Ala His Trp Leu Ala
92 305 310 315 320
93 Phe Phe His Ser Ser Ala Asn Pro Ile Ile Tyr Gly Tyr Phe Asn Glu
94 325 330 335

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97      Pro Pro Trp Ala Ala His Lys Gln Ala Tyr Ser Glu Arg Pro Asn Arg
98              355                      360                      365
99      Leu Leu Arg Arg Arg Val Val Val Asp Val Gln Pro Ser Asp Ser Gly
100             370                      375                      380
101      Leu Pro Ser Glu Ser Gly Pro Ser Ser Gly Val Pro Gly Pro Gly Arg
102             385                      390                      395                      400
103      Leu Pro Leu Arg Asn Gly Arg Val Ala His Gln Asp Gly Pro Gly Glu
104             405                      410                      415
105      Gly Pro Gly Cys Asn His Met Pro Leu Thr Ile Pro Ala Trp Asn Ile
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117      <211> LENGTH: 66
118      <212> TYPE: PRT
119      <213> ORGANISM: Homo sapiens
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124              20              25              30
125      Tyr Gln His Thr Ser Pro Val Ala Ala Met Phe Ile Val Ala Tyr Ala
126              35              40              45
127      Leu Ile Phe Leu Leu Cys Met Val Gly Asn Thr Leu Val Cys Phe Ile
128              50              55              60
129      Val Leu
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133      <212> TYPE: DNA
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138      aatattacct atgtgaacta ctatcttcac cagcctcaag tggcagcaat cttcattatt 180
139      tcctactttc tgatcttctt tttgtgcatg atgggaaata ctgtgggttg ctttattgta 240
140      atgaggaaca aacatatgca cacagtcact aatctcttca tcttaaacct ggccataagt 300
141      gatttactag ttggcatatt ctgcatgcct ataactctgc tggacaatat tatagcagga 360
142      tggccatttg gaaacacgat gtgcaagatc agtggattgg tccagggaaat atctgtcgca 420
143      gcttcagtct ttacgttagt tgcaattgct gtagataggt tccagtgtgt ggtctaccct 480
144      tttaaacc aa agctcactat caagacagcg tttgtcatta ttatgatcat ctgggtccta 540

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147 ccaaatcagg aaatgaggaa gatctacacc actgtgctgt ttgccaatct ctacctggct 720
148 cccctctccc tcattgtcat catgtatgga aggattggaa ttctactctt cagggctgca 780
149 gttcctcaca caggcaggaa gaaccaggag cagtggcacg tgggtgtccag gaagaagcag 840
150 aagatcatta agatgctcct gattgtggcc ctgcttttta ttctctcatg gctgcccctg 900
151 tggactctaa tgatgctctc agactacgct gacctttctc caaatgaact gcagatcatc 960
152 aacatctaca tctacccttt tgcacactgg ctggcattcg gcaacagcag tgtcaatccc 1020
153 atcatttatg gtttcttcaa cgagaatttc cgccgtgggt tccaagaagc tttccagctc 1080
154 cagctctgcc aaaaaagagc aaagcctatg gaagcttatg ccctaaaagc taaaagccat 1140
155 gtgctcataa acacatctaa tcagcttgctc caggaatcta catttcaaaa ccctcatggg 1200
156 gaaaccttgc tttataggaa aagtgtgtaa aaacccaac aggaattagt gatggaagaa 1260
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162 <400> SEQUENCE: 6

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167 Thr Tyr Val Asn Tyr Tyr Leu His Gln Pro Gln Val Ala Ala Ile Phe
168 35 40 45
169 Ile Ile Ser Tyr Phe Leu Ile Phe Phe Leu Cys Met Met Gly Asn Thr
170 50 55 60
171 Val Val Cys Phe Ile Val Met Arg Asn Lys His Met His Thr Val Thr
172 65 70 75 80
173 Asn Leu Phe Ile Leu Asn Leu Ala Ile Ser Asp Leu Leu Val Gly Ile
174 85 90 95
175 Phe Cys Met Pro Ile Thr Leu Leu Asp Asn Ile Ile Ala Gly Trp Pro
176 100 105 110
177 Phe Gly Asn Thr Met Cys Lys Ile Ser Gly Leu Val Gln Gly Ile Ser
178 115 120 125
179 Val Ala Ala Ser Val Phe Thr Leu Val Ala Ile Ala Val Asp Arg Phe
180 130 135 140
181 Gln Cys Val Val Tyr Pro Phe Lys Pro Lys Leu Thr Ile Lys Thr Ala
182 145 150 155 160
183 Phe Val Ile Ile Met Ile Ile Trp Val Leu Ala Ile Thr Ile Met Ser
184 165 170 175
185 Pro Ser Ala Val Met Leu His Val Gln Glu Glu Lys Tyr Tyr Arg Val
186 180 185 190
187 Arg Leu Asn Ser Gln Asn Lys Thr Ser Pro Val Tyr Trp Cys Arg Glu
188 195 200 205
189 Asp Trp Pro Asn Gln Glu Met Arg Lys Ile Tyr Thr Thr Val Leu Phe
190 210 215 220
191 Ala Asn Ile Tyr Leu Ala Pro Leu Ser Leu Ile Val Ile Met Tyr Gly
192 225 230 235 240
193 Arg Ile Gly Ile Ser Leu Phe Arg Ala Ala Val Pro His Thr Gly Arg
194 245 250 255

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198                      275                      280                      285
199      Pro Leu Trp Thr Leu Met Met Leu Ser Asp Tyr Ala Asp Leu Ser Pro
200                      290                      295                      300
201      Asn Glu Leu Gln Ile Ile Asn Ile Tyr Ile Tyr Pro Phe Ala His Trp
202      305                      310                      315                      320
203      Leu Ala Phe Gly Asn Ser Ser Val Asn Pro Ile Ile Tyr Gly Phe Phe
204                      325                      330                      335
205      Asn Glu Asn Phe Arg Arg Gly Phe Gln Glu Ala Phe Gln Leu Gln Leu
206                      340                      345                      350
207      Cys Gln Lys Arg Ala Lys Pro Met Glu Ala Tyr Ala Leu Lys Ala Lys
208                      355                      360                      365
209      Ser His Val Leu Ile Asn Thr Ser Asn Gln Leu Val Gln Glu Ser Thr
210                      370                      375                      380
211      Phe Gln Asn Pro His Gly Glu Thr Leu Leu Tyr Arg Lys Ser Ala Glu
212      385                      390                      395                      400
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220 <213> ORGANISM: Homo sapiens
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224      cctgtggcgg ccatgttcat tgtggcctat gcgtcatct tctgtctctg catggtgggc 180
225      aacacccctg tctgtttcat cgtgtcaag aaccggcaca tgcatactgt caccaacatg 240
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231      accgtcaccg gtgaggagca ccacttcatg gtggacgccc gcaaccgctc ctacctctc 600
232      tactcctgct gggaggcctg gcccgagaag ggcacgcgca ggggtctacac cactgtgctc 660
233      ttctcgaca tctacctggc gccgctggcg ctcatcgtgg tcatgtacgc ccgcatcgcg 720
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236      ctgtcctggc tgccgctctg ggcgtgctg ctgctcatcg actacgggca gtcacgcgcg 900
237      ccgcagctgc acctggtcac cgtctacgcc ttcccttcg cgcactggct ggccttcttc 960
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Line ? Error/Warning

Original Text

312 W "N" or "Xaa" used: Feature required

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322 W "N" or "Xaa" used: Feature required

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